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1600

RAW SEQUENCE LISTING

DATE: 05/07/2002

PATENT APPLICATION: US/09/441,966A

TIME: 14:28:10

Input Set : A:\09-441,966 sequence listing.txt

Output Set: N:\CRF3\05072002\I441966A.raw

p.6

ENTERED

3 <110> APPLICANT: Hall, Roderick L.
4 Poll, Christopher T.
5 Newton, Benjamin B.
6 Taylor, William J.A.
8 <120> TITLE OF INVENTION: Method For Accelerating The Rate of Mucociliary Clearance
10 <130> FILE REFERENCE: 98-736-A
12 <140> CURRENT APPLICATION NUMBER: US 09/441,966A
13 <141> CURRENT FILING DATE: 1999-11-17
15 <150> PRIOR APPLICATION NUMBER: US 09/218,913
16 <151> PRIOR FILING DATE: 1998-12-22
18 <160> NUMBER OF SEQ ID NOS: 105
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 179
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
29 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
30 1 5 10 15
33 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
34 20 25 30
37 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
38 35 40 45
41 Asn Asn Tyr Leu Thr Lys Glu Cys Leu Lys Lys Cys Ala Thr Val
42 50 55 60
45 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
46 65 70 75 80
49 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
50 85 90 95
53 Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr
54 100 105 110
57 Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg
58 115 120 125
61 Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn
62 130 135 140
65 Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
66 145 150 155 160
69 Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
70 165 170 175
73 Ala Val Ser
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 197
79 <212> TYPE: PRT

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80 <213> ORGANISM: Homo sapiens
82 <220> FEATURE:
83 <221> NAME/KEY: SIGNAL
84 <222> LOCATION: (1)..(18)
85 <223> OTHER INFORMATION:
88 <400> SEQUENCE: 2
90 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val
91 1 5 10 15
94 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
95 20 25 30
98 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
99 35 40 45
102 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
103 50 55 60
106 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
107 65 70 75 80
110 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
111 85 90 95
114 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
115 100 105 110
118 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala
119 115 120 125
122 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val
123 130 135 140
126 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn
127 145 150 155 160
130 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg
131 165 170 175
134 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu
135 180 185 190
138 Ala Gly Ala Val Ser
139 195
142 <210> SEQ ID NO: 3
143 <211> LENGTH: 153
144 <212> TYPE: PRT
145 <213> ORGANISM: Homo sapiens
147 <400> SEQUENCE: 3
149 Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala
150 1 5 10 15
153 Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu
154 20 25 30
157 Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys
158 35 40 45
161 Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly
162 50 55 60
165 Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala
166 65 70 75 80
169 Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr
170 85 90 95

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173 Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser
174           100                      105                      110
177 Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe
178           115                      120                      125
181 Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu
182           130                      135                      140
185 Ala Cys Met Leu Arg Cys Phe Arg Gln
186 145                      150
189 <210> SEQ ID NO: 4
190 <211> LENGTH: 58
191 <212> TYPE: PRT
192 <213> ORGANISM: Homo sapiens
194 <400> SEQUENCE: 4
196 Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala
197 1           5                      10                      15
200 Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu
201           20                      25                      30
204 Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys
205           35                      40                      45
208 Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
209           50                      55
212 <210> SEQ ID NO: 5
213 <211> LENGTH: 51
214 <212> TYPE: PRT
215 <213> ORGANISM: Homo sapiens
217 <400> SEQUENCE: 5
219 Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg
220 1           5                      10                      15
223 Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly
224           20                      25                      30
227 Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu
228           35                      40                      45
231 Lys Lys Cys
232           50
235 <210> SEQ ID NO: 6
236 <211> LENGTH: 58
237 <212> TYPE: PRT
238 <213> ORGANISM: Homo sapiens
240 <400> SEQUENCE: 6
242 Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala
243 1           5                      10                      15
246 Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn
247           20                      25                      30
250 Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu
251           35                      40                      45
254 Glu Ala Cys Met Leu Arg Cys Phe Arg Gln
255           50                      55
258 <210> SEQ ID NO: 7
259 <211> LENGTH: 51

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260 <212> TYPE: PRT
261 <213> ORGANISM: Homo sapiens
263 <400> SEQUENCE: 7
265 Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg
266 1          5          10          15
269 Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly
270          20          25          30
273 Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met
274          35          40          45
277 Leu Arg Cys
278          50
281 <210> SEQ ID NO: 8
282 <211> LENGTH: 92
283 <212> TYPE: PRT
284 <213> ORGANISM: Homo sapiens
286 <400> SEQUENCE: 8
288 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
289 1          5          10          15
292 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
293          20          25          30
296 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
297          35          40          45
300 Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
301          50          55          60
304 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
305 65          70          75          80
308 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser
309          85          90
312 <210> SEQ ID NO: 9
313 <211> LENGTH: 708
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Consensus DNA sequence of human Bikunin (Fig. 3).
320 <220> FEATURE:
321 <221> NAME/KEY: misc_feature
322 <222> LOCATION: (679)..(679)
323 <223> OTHER INFORMATION: "n" is any nucleotide.
326 <220> FEATURE:
327 <221> NAME/KEY: misc_feature
328 <222> LOCATION: (707)..(707)
329 <223> OTHER INFORMATION: "n" is any nucleotide.
332 <400> SEQUENCE: 9
333 ggccggggtcg tttctgcct ggctgggata gctgctcctc tctgggggtcc tggcggccga      60
335 ccgagaacgc agcatccacg acttctgcct ggtgtcgaa gttgtgggca gatgccgggc      120
337 ctccatgcct aggtggtggt acaatgtcac tgacggatcc tgccagctgt ttgtgtatgg      180
339 gggctgtgac ggaaacagca ataattacct gaccaaggag gagtgcctca agaaatgtgc      240
341 cactgtcaca gagaatgccg cgggtgacct ggccaccagc aggaatgcag cggattcctc      300
343 tgtcccaagt gctcccagaa ggcaggattc tgaagaccac tccagcgata tgttcaacta      360

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345 tgaagaatac tgcaccgcca acgcagtcac tgggccttgc cgtgcatcct tcccacgctg 420
 347 gtactttgac gtggagagga actcctgcaa taacttcatc tatggaggct gccggggcaa 480
 349 taagaacagc taccgctctg aggaggcctg catgctccgc tgcttccgcc agcaggagaa 540
 351 tcctccccctg ccccttggtg caaagggtggg ggttctggcc ggggctgttt cgtgatggtg 600
 353 ttgatccttt tcctggggag catccatggt ctactgatt ccgggtggca aggaggaacc 660
 355 **aggagcgtgc cctgcgganc gtctggagct tcggagatga caagggnt** 708
 358 <210> SEQ ID NO: 10
 359 <211> LENGTH: 197
 360 <212> TYPE: PRT
 361 <213> ORGANISM: Artificial Sequence
 363 <220> FEATURE:
 364 <223> OTHER INFORMATION: Amino acids -18 to 179 of translation of consensus sequence
 in Fig. 3.
 366 <400> SEQUENCE: 10
 368 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val
 369 1 5 10 15
 372 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
 373 20 25 30
 376 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
 377 35 40 45
 380 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
 381 50 55 60
 384 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
 385 65 70 75 80
 388 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
 389 85 90 95
 392 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
 393 100 105 110
 396 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala
 397 115 120 125
 400 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val
 401 130 135 140
 404 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn
 405 145 150 155 160
 408 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg
 409 165 170 175
 412 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu
 413 180 185 190
 416 Ala Gly Ala Val Ser
 417 195
 420 <210> SEQ ID NO: 11
 421 <211> LENGTH: 179
 422 <212> TYPE: PRT
 423 <213> ORGANISM: Artificial Sequence
 425 <220> FEATURE:
 426 <223> OTHER INFORMATION: Variants of human Bikunin.
 428 <220> FEATURE:
 429 <221> NAME/KEY: MISC_FEATURE
 430 <222> LOCATION: (8)..(8)
 431 <223> OTHER INFORMATION: Each "Xaa" independently represents a naturally occurring
 amino

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/441,966A

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Input Set : A:\09-441,966 sequence listing.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 679,707
Seq#:11; Xaa Pos. 8,17,19,21,22,23,24,25,26,40,42,45,46,47,52,64,103,112
Seq#:11; Xaa Pos. 114,116,117,118,119,120,121,135,137,140,141,142,147,159
Seq#:12; N Pos. 361,367,384,390
Seq#:14; N Pos. 424,481,509
Seq#:16; N Pos. 3,11,12,17,48,425
Seq#:17; N Pos. 6,401,407
Seq#:48; N Pos. 1358
Seq#:51; N Pos. 46,117,313
Seq#:72; Xaa Pos. 9,11,17,19
Seq#:74; Xaa Pos. 25
Seq#:75; N Pos. 425,482,510
Seq#:76; Xaa Pos. 25
Seq#:77; N Pos. 45,49,118,231,305
Seq#:78; N Pos. 117,123,321
Seq#:79; N Pos. 9,11,222,231,262,267,274
Seq#:80; N Pos. 44,46,76,114,187,268,309,317,332,370
Seq#:81; N Pos. 35,148,235,261,272,293,300,313,320
Seq#:82; N Pos. 56,137,145,159,233
Seq#:83; N Pos. 20,26,95,292,313,314,315
Seq#:84; N Pos. 27,139,223,232,302,310,322,328,357,375,392,398,405,427,437
Seq#:84; N Pos. 449,458,474
Seq#:85; N Pos. 361,367,384,390
Seq#:86; N Pos. 3,11,12,17,48,425
Seq#:87; N Pos. 7,403,409
Seq#:88; N Pos. 48,62,211,232,245,309,318
Seq#:89; N Pos. 424,481,509
Seq#:90; N Pos. 257
Seq#:91; N Pos. 19,147
Seq#:92; N Pos. 33,55,213,228,259,267,324,333,344,387
Seq#:93; N Pos. 306,328,342,365,370,377,382,402
Seq#:94; N Pos. 1,142,339,347
Seq#:95; N Pos. 334,368,376
Seq#:96; N Pos. 108,261
Seq#:97; N Pos. 20,30
Seq#:98; N Pos. 45,102,105,159,174,213,337
Seq#:100; N Pos. 304,309
Seq#:101; N Pos. 24
Seq#:102; N Pos. 61,74,122,184
Seq#:103; N Pos. 7
Seq#:104; N Pos. 32,67,136
Seq#:105; N Pos. 13,19,107